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19425

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: JOYCE, JAMES G.
GEORGE, HUGH A.
HOFMANN, KATHRYN J.
JANSEN, KATHRIN U.
NEEPER, MICHAEL P.

(ii) TITLE OF THE INVENTION: RECOMBINANT PAPILLOMAVIRUS TYPE 18
VACCIUNE

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC.
(B) STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
(C) CITY: RAHWAY
(D) STATE: NJ
(E) COUNTRY: US
(F) ZIP: 07065-0907

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/409,122
(B) FILING DATE: 22-MAR-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CARTY, CHRISTINE E
(B) REGISTRATION NUMBER: 36,099
(C) REFERENCE/DOCKET NUMBER: 19425

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 908-594-6734
(B) TELEFAX: 908-594-4720
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 1524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCTTTGT GCGGCCTAG TGACAATACC GTATACCTTC CACCTCCTTC TGTGGCAAGA 60
GTTGTAAATA CTGATGATTA TGTGACTCGC ACAAGCATAT TTTATCATGC TGGCAGCTCT 120
AGATTATTAA CTGTTGGTAA TCCATATTTT AGGGTTCCCTG CAGGTGGTGG CAATAAGCAG 180
GATATTCCTA AGGTTTCTGC ATACCAATAT AGAGTATTTT GGGTGCAGTT ACCTGACCCA 240
AATAAATTTG GTTTACCTGA TAATAGTATT TATAATCCTG AAACACAACG TTTAGTGTGG 300
GCCTGTGCTG GAGTGGAAAT TGGCCGTGGT CAGCCTTTAG GTGTTGGCCT TAGTGGGCAT 360
CCATTTTATA ATAAATTAGA TGACACTGAA AGTTCCCATG CCGCTACGTC TAATGTTTCT 420
GAGGACGTTA GGGACAATGT GTCTGTAGAT TATAAGCAGA CACAGTTATG TATTTTGGGC 480
TGTGCCCCCTG CTATTGGGGA ACACTGGGCT AAAGGCACTG CTTGTAAATC GCGTCCTTTA 540
TCACAGGGCG ATTGCCCCC TTTAGAACTT AAGAACACAG TTTTGGAAGA TGGTGATATG 600
GTAGATACTG GATATGGTGC CATGGACTTT AGTACATTGC AAGATACTAA ATGTGAGGTA 660
CCATTGGATA TTTGTGAGTC TATTTGTAAA TATCCTGATT ATTTACAAAT GTCTGCAGAT 720
CCTTATGGGG ATTCCATGTT TTTTGTGCTTA CGACGTGAGC AGCTTTTTGC TAGGCATTTT 780
TGGAATAGGG CAGGTACTAT GGGTGACACT GTGCCCTCAAT CCTTATATAT TAAAGGCACA 840
GGTATGCGTG CTTACCTGG CAGCTGTGTG TATTCTCCCT CTCCAAGTGG CTCTATTGTT 900
ACCTCTGACT CCCAGTTGTT TAATAAACCA TATTGGTTAC ATAAGGCACA GGGTCATAAC 960
AATGGTATCT GCTGGCATAA TCAATTATTT GTTACTGTGG TAGATACCAC TCGTAGTACC 1020
AATTTAACAA TATGTGCTTC TACACAGTCT CCTGTACCTG GGCAATATGA TGCTACCAAA 1080
TTTAAGCAGT ATAGCAGACA TGTGAAGAA TATGATTTGC AGTTTATTTT TCAGTTATGT 1140
ACTATTACTT TAACTGCAGA TGTATGTGCC TATATTCATA GTATGAATAG CAGTATTTTA 1200
GAGGATTGGA ACTTTGGTGT TCCCCCCCCG CCAACTACTA GTTTGGTGGA TACATATCGT 1260
TTTGTACAAT CTGTTGCTAT TACCTGTCAA AAGGATGCTG CACCAGCTGA AAATAAGGAT 1320
CCCTATGATA AGTTAAAGTT TTGGAATGTG GATTTAAAGG AAAAGTTTTT TTTGGACTTA 1380
GATCAATATC CCCTTGGACG TAAATTTTTG GTTCAGGCTG GATTGCGTCG CAAGCCCACC 1440
ATAGGCCCTC GTAAACGTTT TGCTCCATCT GCCACTACGT CTTCTAAACC TGCCAAGCGT 1500
GTGCGTGAC GTGCCAGGAA GTAA 1524

36

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Leu Trp Arg Pro Ser Asp Asn Thr Val Tyr Leu Pro Pro Pro
 1 5 10 15
 Ser Val Ala Arg Val Val Asn Thr Asp Asp Tyr Val Thr Arg Thr Ser
 20 25 30
 Ile Phe Tyr His Ala Gly Ser Ser Arg Leu Leu Thr Val Gly Asn Pro
 35 40 45
 Tyr Phe Arg Val Pro Ala Gly Gly Gly Asn Lys Gln Asp Ile Pro Lys
 50 55 60
 Val Ser Ala Tyr Gln Tyr Arg Val Phe Arg Val Gln Leu Pro Asp Pro
 65 70 75 80
 Asn Lys Phe Gly Leu Pro Asp Asn Ser Ile Tyr Asn Pro Glu Thr Gln
 85 90 95
 Arg Leu Val Trp Ala Cys Ala Gly Val Glu Ile Gly Arg Gly Gln Pro
 100 105 110
 Leu Gly Val Gly Leu Ser Gly His Pro Phe Tyr Asn Lys Leu Asp Asp
 115 120 125
 Thr Glu Ser Ser His Ala Ala Thr Ser Asn Val Ser Glu Asp Val Arg
 130 135 140
 Asp Asn Val Ser Val Asp Tyr Lys Gln Thr Gln Leu Cys Ile Leu Gly
 145 150 155 160
 Cys Ala Pro Ala Ile Gly Glu His Trp Ala Lys Gly Thr Ala Cys Lys
 165 170 175
 Ser Arg Pro Leu Ser Gln Gly Asp Cys Pro Pro Leu Glu Leu Lys Asn
 180 185 190
 Thr Val Leu Glu Asp Gly Asp Met Val Asp Thr Gly Tyr Gly Ala Met

195 200 205
 Asp Phe Ser Thr Leu Gln Asp Thr Lys Cys Glu Val Pro Leu Asp Ile
 210 215 220
 Cys Gln Ser Ile Cys Lys Tyr Pro Asp Tyr Leu Gln Met Ser Ala Asp
 225 230 235 240
 Pro Tyr Gly Asp Ser Met Phe Phe Cys Leu Arg Arg Glu Gln Leu Phe
 245 250 255
 Ala Arg His Phe Trp Asn Arg Ala Gly Thr Met Gly Asp Thr Val Pro
 260 265 270
 Gln Ser Leu Tyr Ile Lys Gly Thr Gly Met Arg Ala Ser Pro Gly Ser
 275 280 285
 Cys Val Tyr Ser Pro Ser Pro Ser Gly Ser Ile Val Thr Ser Asp Ser
 290 295 300
 Gln Leu Phe Asn Lys Pro Tyr Trp Leu His Lys Ala Gln Gly His Asn
 305 310 315 320
 Asn Gly Ile Cys Trp His Asn Gln Leu Phe Val Thr Val Val Asp Thr
 325 330 335
 Thr Arg Ser Thr Asn Leu Thr Ile Cys Ala Ser Thr Gln Ser Pro Val
 340 345 350
 Pro Gly Gln Tyr Asp Ala Thr Lys Phe Lys Gln Tyr Ser Arg His Val
 355 360 365
 Glu Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Thr Ile Thr Leu
 370 375 380
 Thr Ala Asp Val Met Ser Tyr Ile His Ser Met Asn Ser Ser Ile Leu
 385 390 395 400
 Glu Asp Trp Asn Phe Gly Val Pro Pro Pro Pro Thr Thr Ser Leu Val
 405 410 415
 Asp Thr Tyr Arg Phe Val Gln Ser Val Ala Ile Thr Cys Gln Lys Asp
 420 425 430
 Ala Ala Pro Ala Glu Asn Lys Asp Pro Tyr Asp Lys Leu Lys Phe Trp
 435 440 445
 Asn Val Asp Leu Lys Glu Lys Phe Ser Leu Asp Leu Asp Gln Tyr Pro
 450 455 460
 Leu Gly Arg Lys Phe Leu Val Gln Ala Gly Leu Arg Arg Lys Pro Thr
 465 470 475 480

Ile Gly Pro Arg Lys Arg Ser Ala Pro Ser Ala Thr Thr Ser Ser Lys

485

490

495

Pro Ala Lys Arg Val Arg Val Arg Ala Arg Lys

500

505

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTATCCC	ACCGTGCCGC	ACGACGCAAA	CGGGCTTCGG	TGACTGACTT	ATATAAAACA	60
TGTAAACAAT	CTGGTACATG	TCCATCTGAT	GTTGTTAATA	AGGTAGAGGG	CACCACGTTA	120
GCAGATAAAA	TATTGCAATG	GTCAAGCCTT	GGTATATTTT	TGGGTGGACT	TGGCATAGGT	180
ACTGGAAGTG	GTACAGGGGG	TCGTACAGGG	TACATTCCAT	TGGGTGGGCG	TTCCAATACA	240
GTTGTGGATG	TCGGTCCTAC	ACGTCCTCCA	GTGGTTATTG	AACCTGTGGG	CCCCACAGAC	300
CCATCTATTG	TTACATTAAT	AGAGGACTCA	AGTGTGTGTA	CATCAGGTGC	ACCTAGGCCT	360
ACTTTTACTG	GCACGTCTGG	GTTTGATATA	ACATCTGCTG	GTACAACTAC	ACCTGCAGTT	420
TTGGATATCA	CACCTTCGTC	TACCTCTGTT	TCTATTTCCA	CAACCAATTT	TACCAATCCT	480
GCATTTTCTG	ATCCGTCCAT	TATTGAAGTT	CCACAAACTG	GGGAGGTGTC	AGGTAATGTA	540
TTTGTGGTA	CCCCTACATC	TGGAACACAT	GGGTATGAAG	AAATACCTTT	ACAAACATTT	600
GCTTCTTCTG	GTACGGGGGA	GGAACCCATT	AGTAGTACCC	CATTGCCTAC	TGTGCGGCGT	660
GTAGCAGGTC	CCCGCCTTTA	CAGTAGGGCC	TACCAACAAG	TGTCTGTGGC	TAACCCTGAG	720
TTTCTTACAC	GTCCATCCTC	TTTAATTACC	TATGACAACC	CGGCCTTTGA	GCCTGTGGAC	780
ACTACATTAA	CATTTGAGCC	TCGTAGTAAT	GTTCCCTGATT	CAGATTTTAT	GGATATTATC	840
CGTTTACATA	GGCCTGCTTT	AACATCCAGG	CGTGGTACTG	TGCGCTTTAG	TAGATTAGGT	900
CAAAGGGCAA	CTATGTTTAC	CCGTAGCGGT	ACACAAATAG	GTGCTAGGGT	TCACTTTTAT	960
CATGATATAA	GTCCTATTGC	ACCCCTCCCCA	GAATATATTG	AACTGCAGCC	TTTAGTATCT	1020
GCCACGGAGG	ACAAATGGCTT	GTTTGATATA	TATGCAGATG	ACATAGACCC	TGCAATGCCT	1080
GTACCATCGC	GTCCTACTAC	CTCCTCTGCA	GTTTCTACAT	ATTGCCCCAC	TATATCATCT	1140
GCCTCTTCCT	ATAGTAATGT	AACGGTCCCT	TTAACCTCCT	CTTGGGATGT	GCCTGTATAC	1200

ACGGGTCCTG ATATTACATT ACCACCTACT ACCTCTGTAT GGCCCATTTGT ATCACCCACA 1260
 GCCCCTGCCT CTACACAGTA TATTGGTATA CATGGTACAC ATTATTATTT GTGGCCATTA 1320
 TATTATTTTA TTCCTAAAAA GCGTAAACGT GTTCCCTATT TTTTTCGAGA TGGCTTTGTG 1380
 GCGGCCTAG 1389

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Ser His Arg Ala Ala Arg Arg Lys Arg Ala Ser Val Thr Asp
 1 5 10 15
 Leu Tyr Lys Thr Cys Lys Gln Ser Gly Thr Cys Pro Ser Asp Val Val
 20 25 30
 Asn Lys Val Glu Gly Thr Thr Leu Ala Asp Lys Ile Leu Gln Trp Ser
 35 40 45
 Ser Leu Gly Ile Phe Leu Gly Gly Leu Gly Ile Gly Thr Gly Ser Gly
 50 55 60
 Thr Gly Gly Arg Thr Gly Tyr Ile Pro Leu Gly Gly Arg Ser Asn Thr
 65 70 75 80
 Val Val Asp Val Gly Pro Thr Arg Pro Pro Val Val Ile Glu Pro Val
 85 90 95
 Gly Pro Thr Asp Pro Ser Ile Val Thr Leu Ile Glu Asp Ser Ser Val
 100 105 110
 Val Thr Ser Gly Ala Pro Arg Pro Thr Phe Thr Gly Thr Ser Gly Phe
 115 120 125
 Asp Ile Thr Ser Ala Gly Thr Thr Thr Pro Ala Val Leu Asp Ile Thr
 130 135 140
 Pro Ser Ser Thr Ser Val Ser Ile Ser Thr Thr Asn Phe Thr Asn Pro
 145 150 155 160

Ala Phe Ser Asp Pro Ser Ile Ile Glu Val Pro Gln Thr Gly Glu Val
165 170 175
Ser Gly Asn Val Phe Val Gly Thr Pro Thr Ser Gly Thr His Gly Tyr
180 185 190
Glu Glu Ile Pro Leu Gln Thr Phe Ala Ser Ser Gly Thr Gly Glu Glu
195 200 205
Pro Ile Ser Ser Thr Pro Leu Pro Thr Val Arg Arg Val Ala Gly Pro
210 215 220
Arg Leu Tyr Ser Arg Ala Tyr Gln Gln Val Ser Val Ala Asn Pro Glu
225 230 235 240
Phe Leu Thr Arg Pro Ser Ser Leu Ile Thr Tyr Asp Asn Pro Ala Phe
245 250 255
Glu Pro Val Asp Thr Thr Leu Thr Phe Glu Pro Arg Ser Asn Val Pro
260 265 270
Asp Ser Asp Phe Met Asp Ile Ile Arg Leu His Arg Pro Ala Leu Thr
275 280 285
Ser Arg Arg Gly Thr Val Arg Phe Ser Arg Leu Gly Gln Arg Ala Thr
290 295 300
Met Phe Thr Arg Ser Gly Thr Gln Ile Gly Ala Arg Val His Phe Tyr
305 310 315 320
His Asp Ile Ser Pro Ile Ala Pro Ser Pro Glu Tyr Ile Glu Leu Gln
325 330 335
Pro Leu Val Ser Ala Thr Glu Asp Asn Gly Leu Phe Asp Ile Tyr Ala
340 345 350
Asp Asp Ile Asp Pro Ala Met Pro Val Pro Ser Arg Pro Thr Thr Ser
355 360 365
Ser Ala Val Ser Thr Tyr Ser Pro Thr Ile Ser Ser Ala Ser Ser Tyr
370 375 380
Ser Asn Val Thr Val Pro Leu Thr Ser Ser Trp Asp Val Pro Val Tyr
385 390 395 400
Thr Gly Pro Asp Ile Thr Leu Pro Pro Thr Ser Val Trp Pro Ile Val
405 410 415
Ser Pro Thr Ala Pro Ala Ser Thr Gln Tyr Ile Gly Ile His Gly Thr
420 425 430

His Tyr Tyr Leu Trp Pro Leu Tyr Tyr Phe Ile Pro Lys Lys Arg Lys

435

440

445

Arg Val Pro Tyr Phe Phe Ala Asp Gly Phe Val Ala Ala

450

455

460

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAAGATCTCA CAAAACAAAA TGGCTTTGTG GCGGCCTAGT G

41

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAAGATCTTT ACTTCCTGGC ACGTACACGC ACACGC

36

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCCCCGGGC ACAAACAAA ATGGTATCCC ACCGTGCCGC ACGAC

45

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCCCCCGGGC TAGGCCGCCA CAAAGCCATC TGC

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAATCCTTAT ATATTAAAGG CACAGGTATG

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATCATATTG CCCAGGTACA GGAGACTGTG

30

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAAGATCTCA CAAAACAAAA TGGCTTTGTG GCGGCCTAGT G

41

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTAACGTCC TCAGAAACAT TAGAC

25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTAAAGCTT ATGTCACTTT CTCTTGATC

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGATAAGCTT GCTCAATGGT TCTCTTCCTC

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCATCCC AAATCTTGAA A

21

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CACCGTAGTG TTTGGAAGCG A

21

45